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SEQUENCE LISTING

<110> Abbott Laboratories
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Huang, Yung-Sheng
Das, Tapas
Thurmond, Jennifer M.
Pereira, Suzette L.
Leonard, Amanda E.

<120> DESATURASE GENES AND USES THEREOF

<130> 6763.US.P1

<140> 10/054,534
<141> 2002-01-22

<150> US 09/769,863
<151> 2001-01-25

B1 <160> 55

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<223> Primer R0834

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<222> (3)...(3)
<223> b = g or c or t/u at position 3

<221> misc_feature
<222> (6)...(6)
<223> y = t/u or c at position 6

<221> misc_feature
<222> (9)...(9)
<223> y = t/u or c at position 9

<221> misc_feature
<222> (12)...(12)
<223> b = g or c or t/u at position 12

<221> misc_difference
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (24)...(24)
<223> b = g or c or t/u at position 24

<221> misc_feature
<222> (30)...(30)
<223> y = t/u or c at position 30

<221> misc_feature
<222> (33)...(33)
<223> y = t/u or c at position 33

<221> misc_feature
<222> (36)...(36)
<223> b = g or c or t/u at position 36

<221> misc_feature
<222> (39)...(39)
<223> h = a or c or t/u at position 39

<221> misc_feature
<222> (42)...(42)
<223> h = a or c or t/u at position 42

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<223> Forward Primer R0835

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<223> y = t/u or c at position 6

<221> misc_feature
<222> (12)...(12)
<223> y = t/u or c at position 12

<221> misc_feature
<222> (27)...(27)
<223> y = t/u or c at position 27

<221> misc_feature
<222> (33)...(33)
<223> y = tu or c at position 33

<221> misc_feature
<222> (39)...(39)
<223> b = g or c or t/u at position 39

<221> misc_feature

<222> (41)...(41)
 <223> y = t/u or c at position 41

<221> misc_feature
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 <223> y = t/u or c at position 45

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45

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 <223> Reverse Primer R0836

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 <223> r = g or a at position 1

<221> misc_feature
 <222> (4)...(4)
 <223> r = g or a at position 4

<221> misc_feature
 <222> (7)...(7)
 <223> v = a or g or c at position 7

<221> misc_feature
 <222> (13)...(13)
 <223> r = g or a at position 13

<221> misc_feature
 <222> (19)...(19)
 <223> r = g or a at position 19

<221> misc_feature
 <222> (34)...(34)
 <223> r = g or a at position 34

<221> misc_feature
 <222> (40)...(40)
 <223> r = g or a at position 40

<221> misc_feature
 <222> (43)...(43)
 <223> d = a or g or t/u at position 43

<400> 3
 rtgrtgvacg ttrtgctgrt gcttcacca gttrgcgar gdc

45

<210> 4
 <211> 36
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Reverse Primer R0838

<221> misc_feature
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<223> r = g or a at position 6

<221> misc_feature
<222> (12)...(12)
<223> r = g or a at position 12

<221> misc_feature
<222> (15)...(15)
<223> y = t/u or c at position 15

<221> misc_feature
<222> (18)...(18)
<223> r = g or a at position 18

<221> misc_feature
<222> (21)...(21)
<223> r = g or a at position 21

<221> misc_feature
<222> (24)...(24)
<223> s = g or c at position 24

<221> misc_feature
<222> (27)...(27)
<223> r = g or a at position 27

<221> misc_feature
<222> (30)...(30)
<223> v = a or g or c at position 30

<400> 4
ttgatrgtgt arctygttgt rgasaarggv tggtag

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer R0753

<221> misc_feature
<222> (10)...(10)
<223> n = a or g or c or t/u, unknown, or other at
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<221> misc_feature
<222> (13)...(13)
<223> r = g or a at position 13

<221> misc_feature

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<222> (16)...(16)
 <223> n = a or g or c or t/u, unknown, or other at
 position 16

<221> misc_feature
 <222> (18)...(19)
 <223> r = g or a at positions 18-19

<221> misc_feature
 <222> (22)...(22)
 <223> r = g or a at position 22

<400> 5
 catcatcatn ggraanarrt grtg

24

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 <223> Primer R0754

<221> misc_feature
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<221> misc_feature
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<221> misc_feature
 <222> (21)...(21)
 <223> n = a or g or c or t/u, unknown, or other at
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<221> misc_feature
 <222> (24)...(24)
 <223> y = t/u or c at position 24

<221> misc_feature
 <222> (27)...(27)
 <223> n = a or g or c or t/u, unknown, or other at
 position 27

<221> misc_feature
 <222> (30)...(30)
 <223> y = t/u or c at position 30

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30

<210> 7
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 <212> DNA
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29

<210> 8
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer R0899

<400> 8
 agcggataac aatttcacac aggaaacagc

30

<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer R0939

<400> 9
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30

<210> 10
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer R0898

<400> 10
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31

<210> 11
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer R0951

<400> 11
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45

<210> 12
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer R0960

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<400> 12
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47

<210> 13
<211> 1362
<212> DNA
<213> Saprolegnia diclina

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caccggggcg gcgtcgatcat gttcacgcag gccggcggaag acgcgaccga tgcgttcgct 180
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cagtcgacgg cggccgtcga cagctcgatc tcggacgagg tcaagaagag ccagtcggac 300
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gccatttgcc tccactttga ctgcacggcc atgtacatgg tcgcggctgt catccttggc 480
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<210> 14
<211> 453
<212> PRT
<213> Saprolegnia diclina

<400> 14
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Glu His Asn Arg Gln Asp Asn Ala Trp Ile Val Ile His His Lys Val
20 25 30
Tyr Asp Ile Ser Ala Phe Glu Asp His Pro Gly Gly Val Val Met Phe
35 40 45
Thr Gln Ala Gly Glu Asp Ala Thr Asp Ala Phe Ala Val Phe His Pro
50 55 60
Ser Ser Ala Leu Lys Leu Leu Glu Gln Tyr Tyr Val Gly Asp Val Asp
65 70 75 80
Gln Ser Thr Ala Ala Val Asp Thr Ser Ile Ser Asp Glu Val Lys Lys
85 90 95
Ser Gln Ser Asp Phe Ile Ala Ser Tyr Arg Lys Leu Arg Leu Glu Val
100 105 110
Lys Arg Leu Gly Leu Tyr Asp Ser Lys Leu Tyr Tyr Leu Tyr Lys
115 120 125
Cys Ala Ser Thr Leu Ser Ile Ala Leu Val Ser Ala Ala Ile Cys Leu

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130	135	140
His Phe Asp Ser Thr Ala Met Tyr Met Val Ala Ala Val Ile Leu Gly		
145	150	155
Leu Phe Tyr Gln Gln Cys Gly Trp Leu Ala His Asp Phe Leu His His		
	165	170
Gln Val Phe Glu Asn His Leu Phe Gly Asp Leu Val Gly Val Met Val		
	180	185
Gly Asn Leu Trp Gln Gly Phe Ser Val Gln Trp Trp Lys Asn Lys His		
	195	200
Asn Thr His His Ala Ile Pro Asn Leu His Ala Thr Pro Glu Ile Ala		
	210	215
Phe His Gly Asp Pro Asp Ile Asp Thr Met Pro Ile Leu Ala Trp Ser		
225	230	235
Leu Lys Met Ala Gln His Ala Val Asp Ser Pro Val Gly Leu Phe Phe		
	245	250
Met Arg Tyr Gln Ala Tyr Leu Tyr Phe Pro Ile Leu Leu Phe Ala Arg		
	260	265
Ile Ser Trp Val Ile Gln Ser Ala Met Tyr Ala Phe Tyr Asn Val Gly		
	275	280
Pro Gly Gly Thr Phe Asp Lys Val Gln Tyr Pro Leu Leu Glu Arg Ala		
	290	295
Gly Leu Leu Leu Tyr Tyr Gly Trp Asn Leu Gly Leu Val Tyr Ala Ala		
305	310	315
Asn Met Ser Leu Leu Gln Ala Ala Ala Phe Leu Phe Val Ser Gln Ala		
	325	330
Ser Cys Gly Leu Phe Leu Ala Met Val Phe Ser Val Gly His Asn Gly		
	340	345
Met Glu Val Phe Asp Lys Asp Ser Lys Pro Asp Phe Trp Lys Leu Gln		
	355	360
Val Leu Ser Thr Arg Asn Val Thr Ser Ser Leu Trp Ile Asp Trp Phe		
	370	375
Met Gly Gly Leu Asn Tyr Gln Ile Asp His His Leu Phe Pro Met Val		
385	390	395
Pro Arg His Asn Leu Pro Ala Leu Asn Val Leu Val Lys Ser Leu Cys		
	405	410
Lys Gln Tyr Asp Ile Pro Tyr His Glu Thr Gly Phe Ile Ala Gly Met		
	420	425
Ala Glu Val Val Val His Leu Glu Arg Ile Ser Ile Glu Phe Phe Lys		
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Glu Phe Pro Ala Met		
450		

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<220>
 <223> Primer R0851

<400> 15
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<210> 16
 <211> 28
 <212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0941

<400> 16

gctgaacggg tggtacgagt cgaacgtg

28

<210> 17

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0953

<400> 17

acgagagaat tcatggcccc gcagacggag ctccgccagc gc

42

<210> 18

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer R0956

<400> 18

aaaagactcg agttagccca tgtggatcgt ggcggcgatg ccctgc

46

<210> 19

<211> 1413

<212> DNA

<213> *Saprolegnia diclina*

<400> 19

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 atcattatcc gcggcaaggc ctacgacgtg accgagtggg ccaacaagca ccccggcggc 180
 cgcgagatgg tgetgctgca cgccggtcgc gaggccaccg acacgttcga ctccgtaccac 240
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 gttggcgagt acttcaagaa gaacaacctc catccgcagg acggcttccc gggcctctgg 420
 cgcgatgatg tcgtgtttgc ggtccggcgc ctccgcttgt acggcatgca cttttcgact 480
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 ctccacgtca tgcacgactc gtccgacgcg tcgtacacca acatgccgtt cttccattac 600
 gtcgtcggcc gctttgccat ggactggttt gccggcggtc cgatgggtgc atggctcaac 660
 cagcacgtcg tgggccacca catctacacg aacgtccgcg gctccgaccc ggatcttccg 720
 gtcaacatgg acggcgacat ccgccgcac gtgaaccgcc aggtgttcca gcccatgtac 780
 gcattccagc acatctacct tccgccgctc tatggcgctg ttggcctcaa gttccgcac 840
 caggacttca ccgacacgtt cggctcgcac acgaacggcc cgatccgcgt caaccgcac 900
 gcgctctcga cgtggatggc catgatcagc tccaagtctg tctgggcctt ctaccgcgtg 960
 taccttccgc ttgccgtgct ccagatgccc atcaagacgt accttgcgat cttcttctc 1020
 gccgagttt tccagggctg gtacctcgcg tccaacttcc aagtaagcca tgtctcgacc 1080
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 ggcgcgctca actaccaggt cgtgcaccac ttgttcccca gcgtgtcgca gtaccactac 1260

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ttgccggact ttacggcggc gttcgttgcc cacttgaagc acctccgcaa catggggccag 1380
cagggcatcg cggccacgat ccacatgggc taa 1413

<210> 20

<211> 470

<212> PRT

<213> Saprolegnia diclina

<400> 20

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His	Asn	Thr	Ala	Ala	Ser	Ala	Trp	Ile	Ile	Ile	Arg	Gly	Lys	Val	Tyr	
	35						40					45				
Asp	Val	Thr	Glu	Trp	Ala	Asn	Lys	His	Pro	Gly	Gly	Arg	Glu	Met	Val	
	50					55					60					
Leu	Leu	His	Ala	Gly	Arg	Glu	Ala	Thr	Asp	Thr	Phe	Asp	Ser	Tyr	His	
65					70					75					80	
Pro	Phe	Ser	Asp	Lys	Ala	Glu	Ser	Ile	Leu	Asn	Lys	Tyr	Glu	Ile	Gly	
			85					90						95		
Thr	Phe	Thr	Gly	Pro	Ser	Glu	Phe	Pro	Thr	Phe	Lys	Pro	Asp	Thr	Gly	
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Phe	Tyr	Lys	Glu	Cys	Arg	Lys	Arg	Val	Gly	Glu	Tyr	Phe	Lys	Lys	Asn	
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Asn	Leu	His	Pro	Gln	Asp	Gly	Phe	Pro	Gly	Leu	Trp	Arg	Met	Met	Val	
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Val	Phe	Ala	Val	Ala	Gly	Leu	Ala	Leu	Tyr	Gly	Met	His	Phe	Ser	Thr	
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Ile	Phe	Ala	Leu	Gln	Leu	Ala	Ala	Ala	Leu	Phe	Gly	Val	Cys	Gln		
			165					170					175			
Ala	Leu	Pro	Leu	Leu	His	Val	Met	His	Asp	Ser	Ser	His	Ala	Ser	Tyr	
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Thr	Asn	Met	Pro	Phe	Phe	His	Tyr	Val	Val	Gly	Arg	Phe	Ala	Met	Asp	
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Trp	Phe	Ala	Gly	Gly	Ser	Met	Val	Ser	Trp	Leu	Asn	Gln	His	Val	Val	
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Gly	His	His	Ile	Tyr	Thr	Asn	Val	Ala	Gly	Ser	Asp	Pro	Asp	Leu	Pro	
225					230					235					240	
Val	Asn	Met	Asp	Gly	Asp	Ile	Arg	Arg	Ile	Val	Asn	Arg	Gln	Val	Phe	
			245						250					255		
Gln	Pro	Met	Tyr	Ala	Phe	Gln	His	Ile	Tyr	Leu	Pro	Pro	Leu	Tyr	Gly	
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Val	Leu	Gly	Leu	Lys	Phe	Arg	Ile	Gln	Asp	Phe	Thr	Asp	Thr	Phe	Gly	
		275					280					285				
Ser	His	Thr	Asn	Gly	Pro	Ile	Arg	Val	Asn	Pro	His	Ala	Leu	Ser	Thr	
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			325					330						335		
Ile	Phe	Phe	Leu	Ala	Glu	Phe	Val	Thr	Gly	Trp	Tyr	Leu	Ala	Phe	Asn	
			340					345					350			
Phe	Gln	Val	Ser	His	Val	Ser	Thr	Glu	Cys	Gly	Tyr	Pro	Cys	Gly	Asp	
		355					360					365				
Glu	Ala	Lys	Met	Ala	Leu	Gln	Asp	Glu	Trp	Ala	Val	Ser	Gln	Val	Lys	

370		375		380											
Thr	Ser	Val	Asp	Tyr	Ala	His	Gly	Ser	Trp	Met	Thr	Thr	Phe	Leu	Ala
385					390					395					400
Gly	Ala	Leu	Asn	Tyr	Gln	Val	Val	His	His	Leu	Phe	Pro	Ser	Val	Ser
			405						410					415	
Gln	Tyr	His	Tyr	Pro	Ala	Ile	Ala	Pro	Ile	Ile	Val	Asp	Val	Cys	Lys
			420					425					430		
Glu	Tyr	Asn	Ile	Lys	Tyr	Ala	Ile	Leu	Pro	Asp	Phe	Thr	Ala	Ala	Phe
	435						440					445			
Val	Ala	His	Leu	Lys	His	Leu	Arg	Asn	Met	Gly	Gln	Gln	Gly	Ile	Ala
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Ala	Thr	Ile	His	Met	Gly										
465					470										

<210> 21
 <211> 914
 <212> DNA
 <213> Homo sapiens

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 tgccggggga ttttagtggt gtataacctt ggactcacac tgctgtctct gtatatgttc 240
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 accgcaggag aatcagatat gaagattatc cgtgtcctct ggtggtaacta cttctccaaa 360
 ctcatagaat ttatggacac tttcttcttc atcctgcgca agaacaacca ccagatcacg 420
 gtccctgcacg tctaccacca tgcctcgatg ctgaacatct ggtggtttgt gatgaactgg 480
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 tccctgattg ctctcttcac aaacttctac attcagacct acaacaagaa aggggcctcc 780
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 agtcaaagaa ttga 914

<210> 22
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 <212> DNA
 <213> Mortierella alpina

<400> 22
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 gccaggccg agaagtacat cccacgatt gtccatcaca cgcgtgggtt cctggctcgcg 180
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 tacatcacgc gctcgcagat gacacagttc tgcattgatg cgggtccagtc ttcctgggac 780

atgtacgcca tgaaggctct tggccgcccc ggatacccct tcttcatcac ggctctgctt 840
 tggttctaca tgtggaccat gctcgggtctc ttctacaact tttacagaaa gaacgccaag 900
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<220>
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41

<210> 28

<211> 1320

<212> DNA

<213> Thraustochytrium aureum

<400> 28

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gcgtttcgcg agtttctactg ccggtcgggc aaggcggaag agtacctcaa gagcctgccc 240
aagctcggcg cgccgagcaa gatgaagttt gacgccaagg agcaggcccg gcgcgacgcg 300
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atcgcgcagg gccgctgcgg ctggctcatg cagcagtgcg gacacttctc gatgaccggg 540
tacatcccg cctgacgtgcg cctgcaggag ctgggtgtacg gcgtgggggtg ctcgatgtcg 600
gcgagctgggt ggcgcgttca gcacaacaag caccacgcga cccgcagaa actcaagcac 660
gacgtcgacc tcgacaccct gccgctcggt gcgttcaacg agaagatcgc cgccaaggtg 720
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<210> 29

<211> 439

<212> PRT

<213> Thraustochytrium aureum

<400> 29

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 20                    25                    30
Asp Val Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Phe Leu
 35                    40                    45
Thr Thr Asp Gly Thr Glu Ala Val Asp Ala Thr Asn Ala Phe Arg Glu
 50                    55                    60
Phe His Cys Arg Ser Gly Lys Ala Glu Lys Tyr Leu Lys Ser Leu Pro
 65                    70                    75                    80
Lys Leu Gly Ala Pro Ser Lys Met Lys Phe Asp Ala Lys Glu Gln Ala
 85                    90                    95
Arg Arg Asp Ala Ile Thr Arg Asp Tyr Val Lys Leu Arg Glu Glu Met
100                    105                    110
Val Ala Glu Gly Leu Phe Lys Pro Ala Pro Leu His Ile Val Tyr Arg
115                    120                    125
Phe Ala Glu Ile Ala Ala Leu Phe Ala Ala Ser Phe Tyr Leu Phe Ser
130                    135                    140
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<213> Thraustochytrium aureum
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ttcaggcatc	ctggttggtc	catcatcaaa	tatttgtgca	ccgatggcaa	ggaggtagtt	240
gatgcaaccg	aagcgtacaa	ggagtccac	tgcagatcct	cgaaggcggt	caagtacctc	300
aactccctgc	caagatcg	cggcccaatc	aagtacaaat	acgacgcaa	ggagcaggct	360
cgccatgaca	aactcacgag	ggagtatgta	gctctccgcg	aacagctcgt	caaggaggga	420
tactttgacc	ccagcccgt	ccacattatc	tacagatg	ccgagttggc	agccatgttc	480
gctctctcgt	tctacctttt	ctccttcaag	ggtaacgtca	tggccactat	tgctgccatc	540
gtgattgggg	ggtgcggtga	gggtcgattg	gggtggctca	tgcgtgaagc	tggccactac	600
agcatgaccg	gaaacatccc	tgttgacttg	cgccctcaag	agtttttgta	cgggaattggg	660
tgtggcatga	gcggggcctg	gtggagaagc	cagcacaaca	agcaccacgc	caccccccaa	720
aaqctcaagc	atgacgttga	tttggacact	cttctctctg	tgcctggaa	cgagaaaatt	

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gcccgtcgcg tcaagccagg tagcttccag gcaaagtggc ttcattctcca gggatacatc 780
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tggtttctcg tttcttttgag catgggctac actgtcggag agtctctggg tctctatgtg 960
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gtcaagaaac ttttcgagga caatggtctg gtatacgacg cccgctcata cgtccaggcg 1260
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<210> 31

<211> 439

<212> PRT

<213> *Thraustochytrium aureum*

<400> 31

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Ser Ser Pro Ser Glu Gln Arg Lys Val Leu Leu Ile Asp Gly Gln Leu
  20          25          30
Tyr Asp Ala Thr Asn Phe Arg His Pro Gly Gly Ser Ile Ile Lys Tyr
  35          40          45
Leu Cys Thr Asp Gly Lys Glu Val Val Asp Ala Thr Glu Ala Tyr Lys
  50          55          60
Glu Phe His Cys Arg Ser Ser Lys Ala Val Lys Tyr Leu Asn Ser Leu
  65          70          75          80
Pro Lys Ile Asp Gly Pro Ile Lys Tyr Lys Tyr Asp Ala Lys Glu Gln
  85          90          95
Ala Arg His Asp Lys Leu Thr Arg Glu Tyr Val Ala Leu Arg Glu Gln
 100          105          110
Leu Val Lys Glu Gly Tyr Phe Asp Pro Ser Pro Leu His Ile Ile Tyr
 115          120          125
Arg Cys Ala Glu Leu Ala Ala Met Phe Ala Leu Ser Phe Tyr Leu Phe
 130          135          140
Ser Phe Lys Gly Asn Val Met Ala Thr Ile Ala Ala Ile Val Ile Gly
 145          150          155          160
Gly Cys Val Gln Gly Arg Cys Gly Trp Leu Met His Glu Ala Gly His
 165          170          175
Tyr Ser Met Thr Gly Asn Ile Pro Val Asp Leu Arg Leu Gln Glu Phe
 180          185          190
Leu Tyr Gly Ile Gly Cys Gly Met Ser Gly Ala Trp Trp Arg Ser Gln
 195          200          205
His Asn Lys His His Ala Thr Pro Gln Lys Leu Lys His Asp Val Asp
 210          215          220
Leu Asp Thr Leu Pro Leu Val Ala Trp Asn Glu Lys Ile Ala Arg Arg
 225          230          235          240
Val Lys Pro Gly Ser Phe Gln Ala Lys Trp Leu His Leu Gln Gly Tyr
 245          250          255
Ile Phe Ala Pro Val Ser Cys Leu Leu Val Gly Leu Phe Trp Thr Leu
 260          265          270
Tyr Leu His Pro Arg His Met Ile Arg Thr Lys Arg Asn Phe Glu Ile
 275          280          285
Phe Ser Val Ala Leu Arg Tyr Val Cys Trp Phe Ser Leu Leu Leu Ser
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[illegible]

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 35 40 45
 Gly Ser Val Ile Lys Tyr Gly Leu Ala Asn Thr Gly Ala Asp Ala Thr
 50 55 60
 Ser Leu Phe Glu Ala Phe His Met Arg Ser Lys Lys Ala Gln Met Val
 65 70 75 80
 Leu Lys Ser Leu Pro Lys Arg Ala Pro Val Leu Glu Ile Gln Pro Asn
 85 90 95
 Gln Leu Pro Glu Glu Gln Thr Lys Glu Ala Glu Met Leu Arg Asp Phe
 100 105 110
 Lys Lys Phe Glu Asp Glu Ile Arg Arg Asp Gly Leu Met Glu Pro Ser
 115 120 125
 Phe Trp His Arg Ala Tyr Arg Leu Ser Glu Leu Val Gly Met Phe Thr
 130 135 140
 Leu Gly Leu Tyr Leu Phe Ser Leu Asn Thr Pro Leu Ser Ile Ala Ala
 145 150 155 160
 Gly Val Leu Val His Gly Leu Phe Gly Ala Phe Cys Gly Trp Cys Gln
 165 170 175
 His Glu Ala Gly His Gly Ser Phe Phe Tyr Ser Leu Trp Trp Gly Lys
 180 185 190
 Arg Val Gln Ala Met Leu Ile Gly Phe Gly Leu Gly Thr Ser Gly Asp
 195 200 205
 Met Trp Asn Met Met His Asn Lys His His Ala Ala Thr Gln Lys Val
 210 215 220
 His His Asp Leu Asp Ile Asp Thr Thr Pro Phe Val Ala Phe Phe Asn
 225 230 235 240
 Thr Ala Phe Glu Lys Asn Arg Trp Lys Gly Phe Ser Lys Ala Trp Val
 245 250 255
 Arg Phe Gln Ala Phe Thr Phe Ile Pro Val Thr Ser Gly Met Ile Val
 260 265 270
 Met Leu Phe Trp Leu Phe Phe Leu His Pro Arg Arg Val Val Gln Lys
 275 280 285
 Lys Asn Phe Glu Glu Gly Phe Trp Met Leu Ser Ser His Ile Val Arg
 290 295 300
 Thr Tyr Leu Phe His Leu Val Thr Gly Trp Glu Ser Leu Ala Ala Cys
 305 310 315 320
 Tyr Leu Val Gly Tyr Trp Ala Cys Met Trp Val Ser Gly Met Tyr Leu
 325 330 335
 Phe Gly His Phe Ser Leu Ser His Thr His Met Asp Ile Val Glu Ala
 340 345 350
 Asp Val His Lys Asn Trp Val Arg Tyr Ala Val Asp His Thr Val Asp
 355 360 365
 Ile Ser Pro Ser Asn Pro Leu Val Cys Trp Val Met Gly Tyr Leu Asn
 370 375 380
 Met Gln Thr Ile His His Leu Trp Pro Ala Met Pro Gln Tyr His Gln
 385 390 395 400
 Val Glu Val Ser Arg Arg Phe Ala Ile Phe Ala Lys Lys His Gly Leu
 405 410 415
 Asn Tyr Arg Val Val Ser Tyr Phe Glu Ala Trp Arg Leu Met Leu Gln
 420 425 430
 Asn Leu Ala Asp Val Gly Ser His Tyr His Glu Asn Gly Val Lys Arg
 435 440 445
 Ala Pro Lys Lys Ala Lys Ala Gln
 450 455

<210> 34
 <211> 1329
 <212> DNA
 <213> Isochrysis galbana

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 atcgatgctg aaaaggagat gatcatcaac ggccgcgtgt atgacgtgtc gtcattttgtg 180
 aagcggcacc caggtgggctc ggtgatcaag ttccagctgg gcgccgacgc gagcgacgcg 240
 tacaacaact ttacagtcgc ctccaagaag gcggacaaga tgctgtattc gctcccgtcc 300
 cggcggggcg agggcgggta cgcccaggac gacatctccc gcgactttga gaagctgcgc 360
 ctcgagctga aggaggaggg ctacttcgag cccaacctgg tgcacgtgag ctacaggtgt 420
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 gggcactact cgctcaccgg caacatcaag atcgaccggc atctgcagat ggccatctat 600
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 Ala Ala Asp Val Thr Val Ser Ser Ile Asp Ala Glu Lys Glu Met Ile
 35 40 45
 Ile Asn Gly Arg Val Tyr Asp Val Ser Ser Phe Val Lys Arg His Pro
 50 55 60
 Gly Gly Ser Val Ile Lys Phe Gln Leu Gly Ala Asp Ala Ser Asp Ala
 65 70 75 80
 Tyr Asn Asn Phe His Val Arg Ser Lys Lys Ala Asp Lys Met Leu Tyr
 85 90 95
 Ser Leu Pro Ser Arg Pro Ala Glu Ala Gly Tyr Ala Gln Asp Asp Ile
 100 105 110
 Ser Arg Asp Phe Glu Lys Leu Arg Leu Glu Leu Lys Glu Glu Gly Tyr
 115 120 125
 Phe Glu Pro Asn Leu Val His Val Ser Tyr Arg Cys Val Glu Val Leu
 130 135 140
 Ala Met Tyr Trp Ala Gly Val Gln Leu Ile Trp Ser Gly Tyr Trp Phe
 145 150 155 160
 Leu Gly Ala Ile Val Ala Gly Ile Ala Gln Gly Arg Cys Gly Trp Leu

$$f_1(x_1, y_1, z_1) = f_2(x_2, y_2, z_2) = f_3(x_3, y_3, z_3) = f_4(x_4, y_4, z_4) = f_5(x_5, y_5, z_5) = f_6(x_6, y_6, z_6) = f_7(x_7, y_7, z_7) = f_8(x_8, y_8, z_8) = f_9(x_9, y_9, z_9) = f_{10}(x_{10}, y_{10}, z_{10}) = f_{11}(x_{11}, y_{11}, z_{11}) = f_{12}(x_{12}, y_{12}, z_{12}) = f_{13}(x_{13}, y_{13}, z_{13}) = f_{14}(x_{14}, y_{14}, z_{14}) = f_{15}(x_{15}, y_{15}, z_{15}) = f_{16}(x_{16}, y_{16}, z_{16}) = f_{17}(x_{17}, y_{17}, z_{17}) = f_{18}(x_{18}, y_{18}, z_{18}) = f_{19}(x_{19}, y_{19}, z_{19}) = f_{20}(x_{20}, y_{20}, z_{20}) = f_{21}(x_{21}, y_{21}, z_{21}) = f_{22}(x_{22}, y_{22}, z_{22}) = f_{23}(x_{23}, y_{23}, z_{23}) = f_{24}(x_{24}, y_{24}, z_{24}) = f_{25}(x_{25}, y_{25}, z_{25}) = f_{26}(x_{26}, y_{26}, z_{26}) = f_{27}(x_{27}, y_{27}, z_{27}) = f_{28}(x_{28}, y_{28}, z_{28}) = f_{29}(x_{29}, y_{29}, z_{29}) = f_{30}(x_{30}, y_{30}, z_{30}) = f_{31}(x_{31}, y_{31}, z_{31}) = f_{32}(x_{32}, y_{32}, z_{32}) = f_{33}(x_{33}, y_{33}, z_{33}) = f_{34}(x_{34}, 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Asn	Tyr	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Thr	Met
1				5					10		

Bj
Caneu